



SEQUENCE LISTING

<110> Odgren, Paul R.
Marks, Sandy C.
Choi, Yongwon

<120> TRANCE REGULATION OF CHONDROCYTE
DIFFERENTIATION

<130> 07917-120001

<140> 09/933,915
<141> 2001-08-20

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<151> 2000-08-18

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<170> FastSEQ for Windows Version 4.0

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aggaggaga gctccgaagc gagagggccg agcgcc atg cgc cgc gcc agc aga 174
Met Arg Arg Ala Ser Arg
1 5

gac tac acc aag tac ctg cgt ggc tcg gag gag atg ggc ggc ggc ccc 222
Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu Met Gly Gly Pro
10 15 20

gga gcc ccg cac gag ggc ccc ctg cac gcc ccg ccg cct gcg ccg 270
Gly Ala Pro His Glu Gly Pro Leu His Ala Pro Pro Pro Pro Ala Pro
25 30 35

cac cag ccc ccc gcc tcc cgc tcc atg ttc gtg gcc ctc ctg ggg 318
His Gln Pro Pro Ala Ala Ser Arg Ser Met Phe Val Ala Leu Leu Gly
40 45 50

ctg ggg ctg ggc cag gtt gtc tgc agc gtc gcc ctg ttc tat ttc 366
Leu Gly Leu Gly Gln Val Val Cys Ser Val Ala Leu Phe Phe Tyr Phe
55 60 65 70

aga gcg cag atg gat cct aat aga ata tca gaa gat ggc act cac tgc 414
Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys
75 80 85



1 MRRASRDYTKYLRGSEEMGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQVVCSVALFFYF
71 RAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRIKQAFQGAVQKELQHIVGSQHI
141 RAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSHKVSISSWYHDRGWAKISNMTFSNGKLIVNQ
211 DGFYLYYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHYSINVGGF
281 FKLRSGEEISIEVSNPSLLPDQDATYFGAFKVRDID (SEQ ID NO:2)

FIG. 2

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act ctg gag agtcaa gat acaaa tta ata cct gat tca tgt agg aga Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg 105 110 115	510
att aaa cag gcc ttt caa gga gct gtg caa aag gaa tta caa cat atc Ile Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile 120 125 130	558
gtt gga tca cag cac atc aga gca gag aaa gcg atg gtg gat ggc tca Val Gly Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser 135 140 145	606
tgg tta gat ctg gcc aag agg agc aag ctt gaa gct cag cct ttt gct Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala 155 160 165	654
cat ctc act att aat gcc acc gac atc cca tct ggt tcc cat aaa gtg His Leu Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val 170 175 180	702
agt ctg tcc tct tgg tac cat gat cgg ggt tgg gcc aag atc tcc aac Ser Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn 185 190 195	750
atg act ttt agc aat gga aaa cta ata gtt aat cag gat ggc ttt tat Met Thr Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr 200 205 210	798
tac ctg tat gcc aac att tgc ttt cga cat cat gaa act tca gga gac Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp 215 220 225	846
cta gct aca gag tat ctt caa cta atg gtg tac gtc act aaa acc agc Leu Ala Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser 235 240 245	894
atc aaa atc cca agt tct cat acc ctg atg aaa gga gga agc acc aag Ile Lys Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys 250 255 260	942
tat tgg tca ggg aat tct gaa ttc cat ttt tat tcc ata aac gtt ggt Tyr Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly 265 270 275	990
gga ttt ttt aag tta cgg tct gga gag gaa atc agc atc gag gtc tcc Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser 280 285 290	1038
aac ccc tcc tta ctg gat ccg gat cag gat gca aca tac ttt ggg gct Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala 295 300 305	1086

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 Phe Lys Val Arg Asp Ile Asp
 315

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agagaacacg cgtatttaca gccagtgaaa gatgttagac tcatagggttg ttacacaatg	1317
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ccgcaaaattt taccttttt ttttttcaa aatagaaaag ttattagttt tttatcagca	2097
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aaaaaaaaaa	2226

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<213> Homo sapiens

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Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met	
35 40 45	
Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val	
50 55 60	
Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser	
65 70 75 80	
Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn	
85 90 95	
Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile	
100 105 110	
Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln	
115 120 125	
Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys	
130 135 140	
Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu	
145 150 155 160	
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro	
165 170 175	
Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly	
180 185 190	
Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val	
195 200 205	
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His	

210	215	220
His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val		
225	230	235
Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met		240
245	250	255
Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe		
260	265	270
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu		
275	280	285
Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp		
290	295	300
Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp		
305	310	315

<210> 3

<211> 192

<212> PRT

<213> Homo Sapiens

<400> 3

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Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr		
35	40	45
Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His		
50	55	60
Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys		
65	70	75
Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys		
85	90	95
Phe Arg His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln		
100	105	110
Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His		
115	120	125
Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu		
130	135	140
Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser		
145	150	155
Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro		
165	170	175
Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp		
180	185	190

<210> 4

<211> 181

<212> PRT

<213> Homo sapiens

<400> 4

Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu		
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Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu		
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Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu		
35	40	45

Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr
 50 55 60
 Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu
 65 70 75 80
 Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala
 85 90 95
 Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys
 100 105 110
 Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp
 115 120 125
 Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
 130 135 140
 Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro
 145 150 155 160
 Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
 165 170 175
 Val Arg Asp Ile Asp
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 <213> Homo sapiens

<400> 5

Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala
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 Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn
 20 25 30
 Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp
 35 40 45
 Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn
 50 55 60
 Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn
 65 70 75 80
 Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr
 85 90 95
 Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser
 100 105 110
 Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn
 115 120 125
 Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu
 130 135 140
 Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu
 145 150 155 160
 Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp
 165 170 175
 Ile Asp

<210> 6
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 <213> Homo sapiens

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20							25							30	
Ser	Gly	Ser	His	Lys	Val	Ser	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly
35							40					45			
Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Phe	Ser	Asn	Gly	Lys	Leu	Ile	Val
50						55					60				
Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His
65					70				75				80		
His	Glu	Thr	Ser	Gly	Asp	Leu	Ala	Thr	Glu	Tyr	Leu	Gln	Leu	Met	Val
					85				90				95		
Tyr	Val	Thr	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Thr	Leu	Met
					100				105				110		
Lys	Gly	Gly	Ser	Thr	Lys	Tyr	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe
					115			120				125			
Tyr	Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ser	Gly	Glu	Glu
					130			135			140				
Ile	Ser	Ile	Glu	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp
145					150				155				160		
Ala	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Arg	Asp	Ile	Asp			
					165				170						

<210> 7
<211> 160
<212> PRT
<213> Homo sapiens

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Ser	Lys	Leu	Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Thr
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Asp	Ile	Pro	Ser	Gly	Ser	His	Lys	Val	Ser	Leu	Ser	Ser	Trp	Tyr	His
35							40					45			
Asp	Arg	Gly	Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Phe	Ser	Asn	Gly	Lys
50							55					60			
Leu	Ile	Val	Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys
65							70					75			80
Phe	Arg	His	His	Glu	Thr	Ser	Gly	Asp	Leu	Ala	Thr	Glu	Tyr	Leu	Gln
85							90					95			
Leu	Met	Val	Tyr	Val	Thr	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His
100							105					110			
Thr	Leu	Met	Lys	Gly	Gly	Ser	Thr	Lys	Tyr	Trp	Ser	Gly	Asn	Ser	Glu
115							120					125			
Gly	Glu	Glu	Ile	Ser	Ile	Glu	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro
130							135					140			
Asp	Gln	Asp	Ala	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Arg	Asp	Ile	Asp
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<213> Homo sapiens

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 20 25 30
 Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu
 35 40 45
 Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe
 50 55 60
 Arg His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu
 65 70 75 80
 Met Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr
 85 90 95
 Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe
 100 105 110
 His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly
 115 120 125
 Glu Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp
 130 135 140
 Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
 145 150 155

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Met Asp Pro Asn Arg Ile Ser	
1 5	

gaa gat ggc act cac tgc att tat aga att ttg aga ctc cat gaa aat Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn	163
10 15 20	

gca gat ttt caa gac aca act ctg gag agt caa gat aca aaa tta ata Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile	211
25 30 35	

cct gat tca tgt agg aga att aaa cag gcc ttt caa gga gct gtg caa Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln	259
40 45 50 55	

aag gaa tta caa cat atc gtt gga tca cag cac atc aga gca gag aaa Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys	307
60 65 70	

gcg atg gtg gat ggc tca tgg tta gat ctg gcc aag agg agc aag ctt Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu	355
75 80 85	

gaa gct cag cct ttt gct cat ctc act att aat gcc acc gac atc cca Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro	403
90 95 100	
tct ggt tcc cat aaa gtg agt ctg tcc tct tgg tac cat gat cgg ggt Ser Gly Ser His Lys Val Ser Leu Ser Trp Tyr His Asp Arg Gly	451
105 110 115	
tgg gcc aag atc tcc aac atg act ttt agc aat gga aaa cta ata gtt Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val	499
120 125 130 135	
aat cag gat ggc ttt tat tac ctg tat gcc aac att tgc ttt cga cat Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His	547
140 145 150	
cat gaa act tca gga gac cta gct aca gag tat ctt caa cta atg gtg His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val	595
155 160 165	
tac gtc act aaa acc agc atc aaa atc cca agt tct cat acc ctg atg Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met	643
170 175 180	
aaa gga gga agc acc aag tat tgg tca ggg aat tct gaa ttc cat ttt Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe	691
185 190 195	
tat tcc ata aac gtt ggt gga ttt ttt aag tta cgg tct gga gag gaa Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu	739
200 205 210 215	
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220 225 230	
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	1796

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aaacctqaaa aaaaaaacaa aaaaaaaaaa 1945

<210> 10
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<213> Homo sapiens

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 Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln
 35 40 45
 Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Ser
 50 55 60
 Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu Asp
 65 70 75 80
 Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu Thr
 85 90 95
 Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu Ser
 100 105 110
 Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Phe
 115 120 125
 Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr
 130 135 140
 Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala Thr
 145 150 155 160
 Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys Ile
 165 170 175
 Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser
 180 185 190
 Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe
 195 200 205
 Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro Ser
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 Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val
 225 230 235 240
 Arg Asp Ile Asp

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<220>
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<222> (39) ... (1886)

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Met Ala Pro Arg Ala Arg
1 5

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Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu Cys Ala Leu Leu Ala			
10	15	20	
cg ^g ct ^g ca ^g gt ^g gct tt ^g ca ^g at ^c gct cc ^a tg ^t ac ^c ag ^t gag a ^a g		152	
Arg Leu Gln Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu Lys			
25	30	35	
ca ^t ta ^t ga ^g ca ^t ct ^g gg ^a cg ^g tg ^c tg ^t aa ^c aa ^a tg ^t ga ^a cc ^a gg ^a a ^a g		200	
His Tyr Glu His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly Lys			
40	45	50	
ta ^c at ^g tc ^t tc ^t aa ^a tg ^c ac ^t ac ^t ac ^c tg ^t gac ag ^t gta tg ^t ct ^g cc ^c		248	
Tyr Met Ser Ser Lys Cys Thr Thr Ser Asp Ser Val Cys Leu Pro			
55	60	65	70
tg ^t gg ^c cc ^g ga ^t ga ^a ta ^c tt ^g ga ^t ag ^c tg ^g aa ^t ga ^a ga ^t aa ^a tg ^c		296	
Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys Cys			
75	80	85	
tt ^g ct ^g ca ^t aa ^a gt ^t tg ^t ga ^t ac ^a gg ^c gg ^c ct ^g gt ^g gg ^c gt ^g gtc		344	
Leu Leu His Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val Val			
90	95	100	
gg ^c gg ^c aa ^c ag ^c ac ^g ac ^c cc ^c cg ^g cg ^c tg ^c gc ^g tg ^c ac ^g gct gg ^g ta ^c		392	
Ala Gly Asn Ser Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly Tyr			
105	110	115	
ca ^c tg ^g ag ^c ca ^g ga ^c tg ^c ga ^g tg ^c tg ^c cg ^c cg ^c aa ^c ac ^c ga ^g tg ^c gc ^g		440	
His Trp Ser Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys Ala			
120	125	130	
cc ^g gg ^c ct ^g gg ^c gg ^c ca ^g ca ^c cc ^g tt ^g ca ^g ct ^c aa ^c aa ^g ga ^c ac ^a gt ^g		488	
Pro Gly Leu Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr Val			
135	140	145	150
tg ^c aa ^a cc ^t tg ^c ct ^t ga ^c gg ^c ta ^c tt ^t tc ^t ga ^t gg ^c tt ^t tc ^t cc ^c ac ^g		536	
Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser Thr			
155	160	165	
ga ^c aa ^a tg ^c ag ^a cc ^c tg ^g ac ^c aa ^c tg ^t ac ^t tt ^c ct ^t gg ^a aa ^g ag ^a ga ^t		584	
Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg Val			
170	175	180	
ga ^a ca ^t ca ^t gg ^g ac ^a ga ^g aa ^a tc ^c ga ^t gg ^c tt ^g tg ^c ag ^t tc ^t tc ^t ct ^g		632	
Glu His His Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser Leu			
185	190	195	
cc ^a gct ag ^a aa ^a cc ^a cc ^a aa ^t ga ^a cc ^c ca ^t gt ^t ta ^c tt ^g cc ^c gg ^t tt ^a		680	
Pro Ala Arg Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro Gly Leu			
200	205	210	
at ^a at ^t ct ^g ct ^t ct ^c tt ^c gg ^c tg ^t tg ^c gt ^g gct gg ^c at ^c at ^c		728	
Ile Ile Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile Ile			
215	220	225	230
tt ^t gg ^c gt ^t tg ^c ta ^t ag ^g aa ^a gg ^g aa ^a gca ct ^c ac ^a gct aa ^t tt ^g		776	

Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn Leu			
235	240	245	
tgg cac tgg atc aat gag gct tgt ggc cgc cta agt gga gat aag gag			824
Trp His Trp Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys Glu			
250	255	260	
tcc tca ggt gac agt tgt gtc agt aca cac acg gca aac ttt ggt cag			872
Ser Ser Gly Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe Gly Gln			
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cag gga gca tgt gaa ggt gtc tta ctg ctg act ctg gag gag aag aca			920
Gln Gly Ala Cys Glu Gly Val Leu Leu Leu Thr Leu Glu Glu Lys Thr			
280	285	290	
ttt cca gaa gat atg tgc tac cca gat caa ggt ggt gtc tgt cag ggc			968
Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln Gly Val Cys Gln Gly			
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acg tgt gta gga ggt ggt ccc tac gca caa ggc gaa gat gcc agg atg			1016
Thr Cys Val Gly Gly Pro Tyr Ala Gln Gly Glu Asp Ala Arg Met			
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ctc tca ttg gtc agc aag acc gag ata gag gaa gac agc ttc aga cag			1064
Leu Ser Leu Val Ser Lys Thr Glu Ile Glu Glu Asp Ser Phe Arg Gln			
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Met Pro Thr Glu Asp Glu Tyr Met Asp Arg Pro Ser Gln Pro Thr Asp			
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Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser Lys Ser Thr Pro Pro Phe			
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tct gaa ccc ctg gag gtg ggg gag aat gac agt tta agc cag tgc ttc			1208
Ser Glu Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln Cys Phe			
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acg ggg aca cag agc aca gtg ggt tca gaa agc tgc aac tgc act gag			1256
Thr Gly Thr Gln Ser Thr Val Gly Ser Glu Ser Cys Asn Cys Thr Glu			
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ccc ctg tgc agg act gat tgg act ccc atg tcc tct gaa aac tac ttg			1304
Pro Leu Cys Arg Thr Asp Trp Thr Pro Met Ser Ser Glu Asn Tyr Leu			
410	415	420	
caa aaa gag gtg gac agt ggc cat tgc ccg cac tgg gca gcc agc ccc			1352
Gln Lys Glu Val Asp Ser Gly His Cys Pro His Trp Ala Ala Ser Pro			
425	430	435	
agc ccc aac tgg gca gat gtc tgc aca ggc tgc cg aac cct cct ggg			1400
Ser Pro Asn Trp Ala Asp Val Cys Thr Gly Cys Arg Asn Pro Pro Gly			
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Glu Asp Cys Glu Pro Leu Val Gly Ser Pro Lys Arg Gly Pro Leu Pro			

455	460	465	470		
cag tgc gcc tat ggc atg ggc ctt ccc cct gaa gaa gaa gcc agc agg Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro Glu Glu Ala Ser Arg 475	480		485	1496	
acg gag gcc aga gac cag ccc gag gat ggg gct gat ggg agg ctc cca Thr Glu Ala Arg Asp Gln Pro Glu Asp Gly Ala Asp Gly Arg Leu Pro 490	495		500	1544	
agc tca gcg agg gca ggt gcc ggg tct gga agc tcc cct ggt ggc cag Ser Ser Ala Arg Ala Gly Ser Gly Ser Ser Pro Gly Gly Gln 505	510		515	1592	
tcc cct gca tct gga aat gtg act gga aac agt aac tcc acg ttc atc Ser Pro Ala Ser Gly Asn Val Thr Gly Asn Ser Asn Ser Thr Phe Ile 520	525		530	1640	
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gtc agc cag acc tcg cag gag ggc gcg gcg gct gcg gag ccc atg Val Ser Gln Thr Ser Gln Glu Gly Ala Ala Ala Ala Ala Glu Pro Met 555	560		565		1736
ggc cgc ccg gtg cag gag gag acc ctg gcg cgc cga gac tcc ttc gcg Gly Arg Pro Val Gln Glu Thr Leu Ala Arg Arg Asp Ser Phe Ala 570	575		580		1784
ggg aac ggc ccg cgc ttc ccg gac ccg tgc ggc ggc ccc gag ggg ctg Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys Gly Pro Glu Gly Leu 585	590		595		1832
cg ^g gag cc ^g gag a ^a g ^c tc ^g agg cc ^g gt ^g c ^a g ^g c ^a g ^g c ^c Arg Glu Pro Glu Lys Ala Ser Arg Pro Val Gln Glu Gln Gly Ala 600	605		610		1880
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Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn						
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Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser						
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Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp						
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Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys						
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Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys						
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Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg						
115	120	125				
Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln						
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Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser						
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Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr						
165	170	175				
Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala						
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Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His						
195	200	205				
Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala						
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Leu Val Ala Ala Ile Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys						
225	230	235	240			
Ala Leu Thr Ala Asn Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg						
245	250	255				
Leu Ser Gly Asp Lys Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His						
260	265	270				
Thr Ala Asn Phe Gly Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu						
275	280	285				
Thr Leu Glu Glu Lys Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln						
290	295	300				
Gly Gly Val Cys Gln Gly Thr Cys Val Gly Gly Pro Tyr Ala Gln						
305	310	315	320			
Gly Glu Asp Ala Arg Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu						
325	330	335				
Glu Asp Ser Phe Arg Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg						
340	345	350				
Pro Ser Gln Pro Thr Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser						

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Lys Ser Thr Pro Pro Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp		
370	375	380
Ser Leu Ser Gln Cys Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu		
385	390	395
Ser Cys Asn Cys Thr Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met		
405	410	415
Ser Ser Glu Asn Tyr Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro		
420	425	430
His Trp Ala Ala Ser Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly		
435	440	445
Cys Arg Asn Pro Pro Gly Glu Asp Cys Glu Pro Leu Val Gly Ser Pro		
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Lys Arg Gly Pro Leu Pro Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro		
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Ala Asp Gly Arg Leu Pro Ser Ser Ala Arg Ala Gly Ala Gly Ser Gly		
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Ser Ser Pro Gly Gly Gln Ser Pro Ala Ser Gly Asn Val Thr Gly Asn		
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530	535	540
Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln Glu Gly Ala Ala		
545	550	555
Ala Ala Ala Glu Pro Met Gly Arg Pro Val Gln Glu Glu Thr Leu Ala		
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Arg Arg Asp Ser Phe Ala Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys		
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ctccccgcgc actagaacga gcaagtata atcaagttac t atg agt ctg cta aac	236
Met Ser Leu Leu Asn	
1	5

tgt gaa aac agc tgt gga tcc agc cag tct gaa agt gac tgc tgt gtg	284
Cys Glu Asn Ser Cys Gly Ser Ser Gln Ser Glu Ser Asp Cys Cys Val	
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20	

gcc atg gcc agc tcc tgt agc gct gta aca aaa gat gat agt gtg ggt	332
Ala Met Ala Ser Ser Cys Ser Ala Val Thr Lys Asp Asp Ser Val Gly	

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tgc ccc atc tgc ttg atg gca tta cga gaa gca gtg caa acg cca tgc Cys Pro Ile Cys Leu Met Ala Leu Arg Glu Ala Val Gln Thr Pro Cys 70 75 80 85			476
ggc cat agg ttc tgc aaa gcc tgc atc ata aaa tca ata agg gat gca Gly His Arg Phe Cys Lys Ala Cys Ile Ile Lys Ser Ile Arg Asp Ala 90 95 100			524
ggt cac aaa tgt cca gtt gac aat gaa ata ctg ctg gaa aat caa cta Gly His Lys Cys Pro Val Asp Asn Glu Ile Leu Glu Asn Gln Leu 105 110 115			572
ttt cca gac aat ttt gca aaa cgt gag att ctt tct ctg atg gtg aaa Phe Pro Asp Asn Phe Ala Lys Arg Glu Ile Leu Ser Leu Met Val Lys 120 125 130			620
tgt cca aat gaa ggt tgt ttg cac aag atg gaa ctg aga cat ctt gag Cys Pro Asn Glu Gly Cys Leu His Lys Met Glu Leu Arg His Leu Glu 135 140 145			668
gat cat caa gca cat tgt gag ttt gct ctt atg gat tgt ccc caa tgc Asp His Gln Ala His Cys Glu Phe Ala Leu Met Asp Cys Pro Gln Cys 150 155 160 165			716
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atc tgt gaa tac tgc aat act ata ctc atc aga gaa cag atg cct aat Ile Cys Glu Tyr Cys Asn Thr Ile Leu Ile Arg Glu Gln Met Pro Asn 215 220 225			908
cat tat gat cta gac tgc cct aca gcc cca att cca tgc aca ttc agt His Tyr Asp Leu Asp Cys Pro Thr Ala Pro Ile Pro Cys Thr Phe Ser 230 235 240 245			956
act ttt ggt tgc cat gaa aag atg cag agg aat cac ttg gca cgc cac Thr Phe Gly Cys His Glu Lys Met Gln Arg Asn His Leu Ala Arg His 250 255 260			1004

cta caa gag aac acc cag tca cac atg aga atg ttg gcc cag gct gtt		1052
Leu Gln Glu Asn Thr Gln Ser His Met Arg Met Leu Ala Gln Ala Val		
265	270	275
cat agt ttg agc gtt ata ccc gac tct ggg tat atc tca gag gtc cg		1100
His Ser Leu Ser Val Ile Pro Asp Ser Gly Tyr Ile Ser Glu Val Arg		
280	285	290
aat ttc cag gaa act att cac cag tta gag ggt cgc ctt gta aga caa		1148
Asn Phe Gln Glu Thr Ile His Gln Leu Glu Gly Arg Leu Val Arg Gln		
295	300	305
gac cat caa atc cgg gag ctg act gct aaa atg gaa act cag agt atg		1196
Asp His Gln Ile Arg Glu Leu Thr Ala Lys Met Glu Thr Gln Ser Met		
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325		
tat gta agt gag ctc aaa cga acc att cga acc ctt gag gac aaa gtt		1244
Tyr Val Ser Glu Leu Lys Arg Thr Ile Arg Thr Leu Glu Asp Lys Val		
330	335	340
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Ala Glu Ile Glu Ala Gln Gln Cys Asn Gly Ile Tyr Ile Trp Lys Ile		
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Gly Asn Phe Gly Met His Leu Lys Cys Gln Glu Glu Glu Lys Pro Val		
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Val Ile His Ser Pro Gly Phe Tyr Thr Gly Lys Pro Gly Tyr Lys Leu		
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Cys Met Arg Leu His Leu Gln Leu Pro Thr Ala Gln Arg Cys Ala Asn		
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Tyr Ile Ser Leu Phe Val His Thr Met Gln Gly Glu Tyr Asp Ser His		
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425	430	435
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Pro Glu Leu Leu Ala Phe Gln Arg Pro Thr Ile Pro Arg Asn Pro Lys		
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475	480	485
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Arg Phe Asp Met Gly Ser Leu Arg Arg Glu Gly Phe Gln Pro Arg Ser		
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His Ile Leu Lys Asp Cys Pro Arg Arg Gln Val Ser Cys Asp Asn Cys		
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225 230 235 240		
Pro Cys Thr Phe Ser Thr Phe Gly Cys His Glu Lys Met Gln Arg Asn		

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Leu Glu Asp Lys Val Ala Glu Ile Glu Ala Gln Gln Cys Asn Gly Ile			
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435	440	445	
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Pro Arg Asn Pro Lys Gly Phe Gly Tyr Val Thr Phe Met His Leu Glu			
465	470	475	480
Ala Leu Arg Gln Arg Thr Phe Ile Lys Asp Asp Thr Leu Leu Val Arg			
485	490	495	
Cys Glu Val Ser Thr Arg Phe Asp Met Gly Ser Leu Arg Arg Glu Gly			
500	505	510	
Phe Gln Pro Arg Ser Thr Asp Ala Gly Val			
515	520		

<210> 15
<211> 2237
<212> DNA
<213> Mus musculus

<400> 15	
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ccgaactccg ggcgcgcgc catgcgcgg gccagccgag actacggcaa gtacctgcgc	180
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ctggggctgg gactgggcca ggtggctgc agcatcgctc tggccatgtt ctggccatgt	360
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ctccatgaaa acgcaggtt gcaggactcg actctggaga gtggaaacac actacctgac	480
tcctgcagga ggtggaaaca agcctttcag gggccgtgc agaaggaaact gcaacacatt	540
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gcccagcgag gcaagcctga gccccagcca ttgcacacc tcaccatcaa tgctgcc	660
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ctgatgaaag gagggagcac gaaaaactgg tcgggcaatt ctgaattcca ctttattcc	960
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gacatagact gagactcatt tcgtggaca tttagcatgga tgcctctagat gtttggaaac	1140
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tcttattct tttaactta atagagtctt cagacttgc aaaactatgc aagcaaaata	1860
aataaataaaa aataaaatga ataccttga taataagttag gatgttggc accaggtgcc	1920
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gctactgaaa tctgtcagga gtatttatgc aattattgaa caggtgtctt ttttacaag	2040
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<210> 16

<211> 316

<212> PRT

<213> Mus musculus

<400> 16

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20	25	30	
Ala Pro Ser Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser			
35	40	45	
Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser			
50	55	60	
Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile			
65	70	75	80
Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu			
85	90	95	
Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro			
100	105	110	
Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys			
115	120	125	
Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala			
130	135	140	
Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu			
145	150	155	160
Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser			
165	170	175	
Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp			
180	185	190	
Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn			
195	200	205	
Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His			

210	215	220	
Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr			
225	230	235	240
Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys			
245	250	255	
Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr			
260	265	270	
Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile			
275	280	285	
Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala			
290	295	300	
Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp			
305	310	315	

<210> 17

<211> 50

<212> DNA

<213> Homo sapiens

<400> 17

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50

<210> 18

<211> 60

<212> DNA

<213> Homo sapiens

<400> 18

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60

<210> 19

<211> 51

<212> DNA

<213> Homo sapiens

<400> 19

ataatcaagt tactatgagt ctgctaaact gtgaaaacag ctgtggatcc a

51